HEPES, pH adjusted to 7.0 with KOH). Cells were centrifuged again as described above and resuspended in 125 µl chilled buffer. Cells were then centrifuged and resuspended two more times in the same HEPES buffer as described above at a volume of 100 µl and 750 µl, respectively. Resuspended cells were then distributed into 40 µl aliquots, quickly frozen in liquid nitrogen, and stored at -80° C.

Please replace the paragraph on page 371, lines 24-29 with the following amended paragraph:

Salt stress assays are intended to find genes that confer better germination, seedling vigor or growth in high salt. Evaporation from the soil surface causes upward water movement and salt accumulation in the upper soil layer where the seeds are placed. Thus, germination normally takes place at a salt concentration much higher than the mean salt concentration [[of]] in the whole soil profile. Plants differ in their tolerance to NaCl depending on their stage of development, therefore seed germination, seedling vigor, and plant growth responses are evaluated.

Please replace the paragraph on page 392, lines 21-24 with the following amended paragraph (note space after "G581" in line 22):

The function of G581 was first studied by knockout analysis. Homozygous plants containing a T-DNA insertion within the first half of the G581_coding region displayed wild-type morphology at all developmental stages. Furthermore, G581 knockout mutant plants behaved similarly to wild type in all physiological and biochemical assays performed.

SK 10/4/06

Please replace the paragraph on page 427, lines 3-6 with the following amended paragraph (note space after "T1" in line 6):

G1792 overexpressing plants showed several mild morphological alterations: leaves were dark green and shiny, and plants bolted, subsequently senesced, slightly later than wild-type controls. Among the T1_ plants, additional morphological variation (not reproduced later in the T2 plants) was observed: many showed reductions in size as well as aberrations in leaf shape, phyllotaxy, and flower development.

Please replace the paragraph on page 456, lines 20-22 with the following amended paragraph (note space after "G2661" on line 20):

The sequence of G2661_was obtained from the *Arabidopsis* genome sequencing project, GenBank accession number AL161746, nid=7327833, based on its sequence similarity within the conserved domain to other bHLH related proteins in *Arabidopsis*.

Please replace the paragraph on page 485, lines 9-20 with the following amended paragraph:

The "one-hybrid" strategy (Li and Herskowitz (1993) *Science* 262: 1870-1874) is used to screen for plant cDNA clones encoding a polypeptide comprising a transcription factor DNA binding domain, a